CRF   ors Corrected by th STIC Syste Branch

Serial Numb r: 10/085,233B

CRF Processing Date: 10/25/02
Edited by: DC
Verified by: DC (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically:
_____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
_____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:
_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:
_____

☑ Deleted: ☑ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____ .

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:
_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:
_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other:
_____
_____
_____

*Examiner: Th above corrections must be communicated to th applicant in th first Office Action. DO NOT send a copy of this form.   3/1/95

OIPE

```
 4 <110> APPLICANT: GLUCKSMANN, MARIA ALEXANDRA
 6 <120> TITLE OF INVENTION: 93870, A HUMAN G-PROTEIN COUPLED
 7       RECEPTOR AND USES THEREFOR
 9 <130> FILE REFERENCE: MPI2001-021P1RCP1M
11 <140> CURRENT APPLICATION NUMBER: 10/085,233B
13 <141> CURRENT FILING DATE: 2002-02-28
15 <150> PRIOR APPLICATION NUMBER: 60/272,677
17 <151> PRIOR FILING DATE: 2001-03-01
19 <160> NUMBER OF SEQ ID NOS: 6
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1684
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (147)...(1085)
32 <223> OTHER INFORMATION: n at position 1384 can be any
33       nucleotide
35 <400> SEQUENCE: 1
36 tcgacaggtg acacaatttt ccaactattc ttctagcaat gattttcaac aattataaaa  60
37 tggaagttgt agactggata agagatgctc agctaaggga gttcctggat ggcctttaga 120
38 ttgatacacc aatcctctga aattgc atg caa aaa tgt gac ttc cca agt atg 173
39                             Met Gln Lys Cys Asp Phe Pro Ser Met
40                              1               5
42 cct ggc cac aat acc tcc agg aat tcc tct tgc gat cct ata gtg aca 221
43 Pro Gly His Asn Thr Ser Arg Asn Ser Ser Cys Asp Pro Ile Val Thr
44  10              15                  20                  25
46 ccc cac tta atc agc ctc tac ttc ata gtg ctt att ggc ggg ctg gtg 269
47 Pro His Leu Ile Ser Leu Tyr Phe Ile Val Leu Ile Gly Gly Leu Val
48                  30                  35                  40
50 ggt gtc att tcc att ctt ttc ctc ctg gtg aaa atg aac acc cgg tca 317
51 Gly Val Ile Ser Ile Leu Phe Leu Leu Val Lys Met Asn Thr Arg Ser
52                  45                  50                  55
54 gtg acc acc atg gcg gtc att aac ttg gtg gtg gtc cac agc gtt ttt 365
55 Val Thr Thr Met Ala Val Ile Asn Leu Val Val Val His Ser Val Phe
56              60                  65                  70
58 ctg ctg aca gtg cca ttt cgc ttg acc tac ctc atc aag aag act tgg 413
59 Leu Leu Thr Val Pro Phe Arg Leu Thr Tyr Leu Ile Lys Lys Thr Trp
60      75                  80                  85
62 atg ttt ggg ctg ccc ttc tgc aaa ttt gtg agt gcc atg ctg cac atc 461
63 Met Phe Gly Leu Pro Phe Cys Lys Phe Val Ser Ala Met Leu His Ile
64  90                  95                  100                 105
```

```
 66 cac atg tac ctc acg ttc cta ttc tat gtg gtg atc ctg gtc acc aga    509
 67 His Met Tyr Leu Thr Phe Leu Phe Tyr Val Val Ile Leu Val Thr Arg
 68             110                 115                 120
 70 tac ctc atc ttc ttc aag tgc aaa gac aaa gtg gaa ttc tac aga aaa    557
 71 Tyr Leu Ile Phe Phe Lys Cys Lys Asp Lys Val Glu Phe Tyr Arg Lys
 72             125                 130                 135
 74 ctg cat gct gtg gct gcc agt gct ggc atg tgg acg ctg gtg att gtc    605
 75 Leu His Ala Val Ala Ala Ser Ala Gly Met Trp Thr Leu Val Ile Val
 76             140                 145                 150
 78 att gtg gta ccc ctg gtt gtc tcc cgg tat gga atc cat gag gaa tac    653
 79 Ile Val Val Pro Leu Val Val Ser Arg Tyr Gly Ile His Glu Glu Tyr
 80     155                 160                 165
 82 aat gag gag cac tgt ttt aaa ttt cac aaa gag ctt gct tac aca tat    701
 83 Asn Glu Glu His Cys Phe Lys Phe His Lys Glu Leu Ala Tyr Thr Tyr
 84 170                 175                 180                 185
 86 gtg aaa atc atc aac tat atg ata gtc att ttt gtc ata gcc gtt gct    749
 87 Val Lys Ile Ile Asn Tyr Met Ile Val Ile Phe Val Ile Ala Val Ala
 88                 190                 195                 200
 90 gtg att ctg ttg gtc ttc cag gtc ttc atc att atg ttg atg gtg cag    797
 91 Val Ile Leu Leu Val Phe Gln Val Phe Ile Ile Met Leu Met Val Gln
 92             205                 210                 215
 94 aag cta cgc cac tct tta cta tcc cac cag gag ttc tgg gct cag ctg    845
 95 Lys Leu Arg His Ser Leu Leu Ser His Gln Glu Phe Trp Ala Gln Leu
 96             220                 225                 230
 98 aaa aac cta ttt ttt ata ggg gtc atc ctt gtt tgt ttc ctt ccc tac    893
 99 Lys Asn Leu Phe Phe Ile Gly Val Ile Leu Val Cys Phe Leu Pro Tyr
100         235                 240                 245
102 cag ttc ttt agg atc tat tac ttg aat gtt gtg acg cat tcc aat gcc    941
103 Gln Phe Phe Arg Ile Tyr Tyr Leu Asn Val Val Thr His Ser Asn Ala
104 250                 255                 260                 265
106 tgt agc agc aag gtt gca ttt tat aac gaa atc ttc ttg agt gta aca    989
107 Cys Ser Ser Lys Val Ala Phe Tyr Asn Glu Ile Phe Leu Ser Val Thr
108                 270                 275                 280
110 gca att agc tgc tat gat ttg ctt ctc ttt gtc ttt ggg gga agc cat   1037
111 Ala Ile Ser Cys Tyr Asp Leu Leu Leu Phe Val Phe Gly Gly Ser His
112                 285                 290                 295
114 tgg ttt aag caa aag ata att ggc tta tgg aat tgt gtt ttg tgc cgt   1085
115 Trp Phe Lys Gln Lys Ile Ile Gly Leu Trp Asn Cys Val Leu Cys Arg
116             300                 305                 310
118 tagccacaaa ctacagtatt catatttgct tcctttatat tgggaataaa atgggtatag 1145
119 gggaggtaag aatggtattt cattacttga tcaaaaccat gccttgatgt acccaaaaca 1205
120 aaaggactat aaaatgcaag agccctcatt gtagtcctta tgggatccct cccatctctg 1265
121 agtgatggcc gtacaaagac cagtgttgtt gaatccacct ggagttgcaa tattacatta 1325
122 ttttccagta cagaatgtct gtgtggccca tgaaagcaac ataggtttta agagttttna 1385
123 gagtttcatt agctcattct aagttcctct gtttgaagca tggtctctta ggttttggac 1445
124 tgaactcaga cctttagttc ttttcatccc acttcaccat aggtaagtaa attctggcca 1505
125 ccacccagct ccaaagacac aaactctcct tcgctaacca ggttagatgt cccattcatc 1565
126 tcatgccctg ataaaaactg ataaggggag agaatagtta aaaatttttc tagggtatca 1625
127 taactctggt aggaagtcat ctgtctagac tcgagcaagc ttatgcatgc atgcggccg   1684
```
W--> (to line 122)

RAW SEQUENCE LISTING   DATE: 10/25/2002
PATENT APPLICATION: US/10/085,233B   TIME: 10:37:57

Input Set : A:\PTO.DC.txt
Output Set: N:\CRF4\10252002\J085233B.raw

```
129 <210> SEQ ID NO: 2
130 <211> LENGTH: 313
131 <212> TYPE: PRT
132 <213> ORGANISM: Homo sapiens
134 <400> SEQUENCE: 2
135 Met Gln Lys Cys Asp Phe Pro Ser Met Pro Gly His Asn Thr Ser Arg
136  1               5                  10                  15
137 Asn Ser Ser Cys Asp Pro Ile Val Thr Pro His Leu Ile Ser Leu Tyr
138             20                  25                  30
139 Phe Ile Val Leu Ile Gly Gly Leu Val Gly Val Ile Ser Ile Leu Phe
140         35                  40                  45
141 Leu Leu Val Lys Met Asn Thr Arg Ser Val Thr Thr Met Ala Val Ile
142     50                  55                  60
143 Asn Leu Val Val Val His Ser Val Phe Leu Leu Thr Val Pro Phe Arg
144 65                  70                  75                  80
145 Leu Thr Tyr Leu Ile Lys Lys Thr Trp Met Phe Gly Leu Pro Phe Cys
146                 85                  90                  95
147 Lys Phe Val Ser Ala Met Leu His Ile His Met Tyr Leu Thr Phe Leu
148             100                 105                 110
149 Phe Tyr Val Val Ile Leu Val Thr Arg Tyr Leu Ile Phe Phe Lys Cys
150         115                 120                 125
151 Lys Asp Lys Val Glu Phe Tyr Arg Lys Leu His Ala Val Ala Ala Ser
152     130                 135                 140
153 Ala Gly Met Trp Thr Leu Val Ile Val Ile Val Val Pro Leu Val Val
154 145                 150                 155                 160
155 Ser Arg Tyr Gly Ile His Glu Glu Tyr Asn Glu Glu His Cys Phe Lys
156             165                 170                 175
157 Phe His Lys Glu Leu Ala Tyr Thr Tyr Val Lys Ile Ile Asn Tyr Met
158             180                 185                 190
159 Ile Val Ile Phe Val Ile Ala Val Ala Val Ile Leu Leu Val Phe Gln
160         195                 200                 205
161 Val Phe Ile Ile Met Leu Met Val Gln Lys Leu Arg His Ser Leu Leu
162     210                 215                 220
163 Ser His Gln Glu Phe Trp Ala Gln Leu Lys Asn Leu Phe Phe Ile Gly
164 225                 230                 235                 240
165 Val Ile Leu Val Cys Phe Leu Pro Tyr Gln Phe Phe Arg Ile Tyr Tyr
166             245                 250                 255
167 Leu Asn Val Val Thr His Ser Asn Ala Cys Ser Ser Lys Val Ala Phe
168             260                 265                 270
169 Tyr Asn Glu Ile Phe Leu Ser Val Thr Ala Ile Ser Cys Tyr Asp Leu
170         275                 280                 285
171 Leu Leu Phe Val Phe Gly Gly Ser His Trp Phe Lys Gln Lys Ile Ile
172     290                 295                 300
173 Gly Leu Trp Asn Cys Val Leu Cys Arg
174 305                 310
176 <210> SEQ ID NO: 3
177 <211> LENGTH: 939
178 <212> TYPE: DNA
179 <213> ORGANISM: Homo sapiens
```

```
181 <220> FEATURE:
182 <221> NAME/KEY: CDS
183 <222> LOCATION: (1)...(939)
185 <400> SEQUENCE: 3
186 atg caa aaa tgt gac ttc cca agt atg cct ggc cac aat acc tcc agg      48
187 Met Gln Lys Cys Asp Phe Pro Ser Met Pro Gly His Asn Thr Ser Arg
188 1               5                   10                  15
190 aat tcc tct tgc gat cct ata gtg aca ccc cac tta atc agc ctc tac      96
191 Asn Ser Ser Cys Asp Pro Ile Val Thr Pro His Leu Ile Ser Leu Tyr
192             20                  25                  30
194 ttc ata gtg ctt att ggc ggg ctg gtg ggt gtc att tcc att ctt ttc     144
195 Phe Ile Val Leu Ile Gly Gly Leu Val Gly Val Ile Ser Ile Leu Phe
196         35                  40                  45
198 ctc ctg gtg aaa atg aac acc cgg tca gtg acc acc atg gcg gtc att     192
199 Leu Leu Val Lys Met Asn Thr Arg Ser Val Thr Thr Met Ala Val Ile
200     50                  55                  60
202 aac ttg gtg gtg gtc cac agc gtt ttt ctg ctg aca gtg cca ttt cgc     240
203 Asn Leu Val Val Val His Ser Val Phe Leu Leu Thr Val Pro Phe Arg
204 65                  70                  75                  80
206 ttg acc tac ctc atc aag aag act tgg atg ttt ggg ctg ccc ttc tgc     288
207 Leu Thr Tyr Leu Ile Lys Lys Thr Trp Met Phe Gly Leu Pro Phe Cys
208                 85                  90                  95
210 aaa ttt gtg agt gcc atg ctg cac atc cac atg tac ctc acg ttc cta     336
211 Lys Phe Val Ser Ala Met Leu His Ile His Met Tyr Leu Thr Phe Leu
212             100                 105                 110
214 ttc tat gtg gtg atc ctg gtc acc aga tac ctc atc ttc ttc aag tgc     384
215 Phe Tyr Val Val Ile Leu Val Thr Arg Tyr Leu Ile Phe Phe Lys Cys
216         115                 120                 125
218 aaa gac aaa gtg gaa ttc tac aga aaa ctg cat gct gtg gct gcc agt     432
219 Lys Asp Lys Val Glu Phe Tyr Arg Lys Leu His Ala Val Ala Ala Ser
220     130                 135                 140
222 gct ggc atg tgg acg ctg gtg att gtc att gtg gta ccc ctg gtt gtc     480
223 Ala Gly Met Trp Thr Leu Val Ile Val Ile Val Val Pro Leu Val Val
224 145                 150                 155                 160
226 tcc cgg tat gga atc cat gag gaa tac aat gag gag cac tgt ttt aaa     528
227 Ser Arg Tyr Gly Ile His Glu Glu Tyr Asn Glu Glu His Cys Phe Lys
228                 165                 170                 175
230 ttt cac aaa gag ctt gct tac aca tat gtg aaa atc atc aac tat atg     576
231 Phe His Lys Glu Leu Ala Tyr Thr Tyr Val Lys Ile Ile Asn Tyr Met
232             180                 185                 190
234 ata gtc att ttt gtc ata gcc gtt gct gtg att ctg ttg gtc ttc cag     624
235 Ile Val Ile Phe Val Ile Ala Val Ala Val Ile Leu Leu Val Phe Gln
236         195                 200                 205
238 gtc ttc atc att atg ttg atg gtg cag aag cta cgc cac tct tta cta     672
239 Val Phe Ile Ile Met Leu Met Val Gln Lys Leu Arg His Ser Leu Leu
240         210                 215                 220
242 tcc cac cag gag ttc tgg gct cag ctg aaa aac cta ttt ttt ata ggg     720
243 Ser His Gln Glu Phe Trp Ala Gln Leu Lys Asn Leu Phe Phe Ile Gly
244 225                 230                 235                 240
```

```
246 gtc atc ctt gtt tgt ttc ctt ccc tac cag ttc ttt agg atc tat tac   768
247 Val Ile Leu Val Cys Phe Leu Pro Tyr Gln Phe Phe Arg Ile Tyr Tyr
248                 245             250             255
250 ttg aat gtt gtg acg cat tcc aat gcc tgt agc agc aag gtt gca ttt   816
251 Leu Asn Val Val Thr His Ser Asn Ala Cys Ser Ser Lys Val Ala Phe
252                 260             265             270
254 tat aac gaa atc ttc ttg agt gta aca gca att agc tgc tat gat ttg   864
255 Tyr Asn Glu Ile Phe Leu Ser Val Thr Ala Ile Ser Cys Tyr Asp Leu
256             275             280             285
258 ctt ctc ttt gtc ttt ggg gga agc cat tgg ttt aag caa aag ata att   912
259 Leu Leu Phe Val Phe Gly Gly Ser His Trp Phe Lys Gln Lys Ile Ile
260         290             295             300
262 ggc tta tgg aat tgt gtt ttg tgc cgt                               939
263 Gly Leu Trp Asn Cys Val Leu Cys Arg
264 305             310
266 <210> SEQ ID NO: 4
267 <211> LENGTH: 356
268 <212> TYPE: PRT
269 <213> ORGANISM: Mus muscalis
271 <400> SEQUENCE: 4
272 Met Glu Ile Pro Ala Val Thr Glu Pro Ser Tyr Asn Thr Val Ala Lys
273 1               5               10              15
274 Asn Asp Phe Met Ser Gly Phe Leu Cys Phe Ser Ile Asn Val Arg Ala
275             20              25              30
276 Phe Gly Ile Thr Val Pro Thr Pro Leu Tyr Ser Leu Val Phe Ile Ile
277         35              40              45
278 Gly Val Ile Gly His Val Leu Val Val Leu Val Leu Ile Gln His Lys
279     50              55              60
280 Arg Leu Arg Asn Met Thr Ser Ile Tyr Leu Phe Asn Leu Ala Ile Ser
281 65              70              75              80
282 Asp Leu Val Phe Leu Ser Thr Leu Pro Phe Trp Val Asp Tyr Ile Met
283             85              90              95
284 Lys Gly Asp Trp Ile Phe Gly Asn Ala Met Cys Lys Phe Val Ser Gly
285         100         .       105             110
286 Phe Tyr Tyr Leu Gly Leu Tyr Ser Asp Met Phe Phe Ile Thr Leu Leu
287         115             120             125
288 Thr Ile Asp Arg Tyr Leu Ala Val Val His Val Val Phe Ala Leu Arg
289     130             135             140
290 Ala Arg Thr Val Thr Phe Gly Ile Ile Ser Ser Ile Ile Thr Trp Val
291 145             150             155             160
292 Leu Ala Ala Leu Val Ser Ile Pro Cys Leu Tyr Val Phe Lys Ser Gln
293             165             170             175
294 Met Glu Phe Thr Tyr His Thr Cys Arg Ala Ile Leu Pro Arg Lys Ser
295             180             185             190
296 Leu Ile Arg Phe Leu Arg Phe Gln Ala Leu Thr Met Asn Ile Leu Gly
297         195             200             205
298 Leu Ile Leu Pro Leu Leu Ala Met Ile Ile Cys Tyr Thr Arg Ile Ile
299     210             215             220
300 Asn Val Leu His Arg Arg Pro Asn Lys Lys Lys Ala Lys Val Met Arg
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 10/25/2002
PATENT APPLICATION: US/10/085,233B   TIME: 10:37:58

Input Set : A:\PTO.DC.txt
Output Set: N:\CRF4\10252002\J085233B.raw

<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 1384
Seq#:6; Xaa Pos. 1,2,3,4,5,6,7,8,9,10,11,12,14,15,16,17

VERIFICATION SUMMARY   DATE: 10/25/2002
PATENT APPLICATION: US/10/085,233B   TIME: 10:37:58

Input Set : **A:\PTO.DC.txt**
Output Set: **N:\CRF4\10252002\J085233B.raw**

```
L:122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1325
L:344 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:349 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:354 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:359 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:364 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:369 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:374 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:379 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:385 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:390 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:395 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:400 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:404 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:409 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:415 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:421 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:425 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:428 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:16
```

OIPE

Does Not Comply
Corrected Diskette Needed

```
                RAW SEQUENCE LISTING            DATE: 10/25/2002
                PATENT APPLICATION:  US/10/085,233B      TIME: 10:31:19

                Input Set : A:\PTO.DC.txt
                Output Set: N:\CRF4\10252002\J085233B.raw

     4 <110> APPLICANT: GLUCKSMANN, MARIA ALEXANDRA
     6 <120> TITLE OF INVENTION: 93870, A HUMAN G-PROTEIN COUPLED
     7        RECEPTOR AND USES THEREFOR
     9 <130> FILE REFERENCE: MPI2001-021P1RCP1M
    11 <140> CURRENT APPLICATION NUMBER: 10/085,233B
    13 <141> CURRENT FILING DATE: 2002-02-28
    15 <150> PRIOR APPLICATION NUMBER: 60/272,677
    17 <151> PRIOR FILING DATE: 2001-03-01
    19 <160> NUMBER OF SEQ ID NOS: 6
    21 <170> SOFTWARE: FastSEQ for Windows Version 4.0


ERRORED SEQUENCES

       336 <210> SEQ ID NO: 6
       337 <211> LENGTH: 17
       338 <212> TYPE: PRT
       339 <213> ORGANISM: Artificial Sequence
       341 <220> FEATURE:
       342 <223> OTHER INFORMATION: Consensus
W--> 344 <221> NAME/KEY: VARIANT
       345 <222> LOCATION: (1)...(1)
       346 <223> OTHER INFORMATION: Xaa at position 1 can be G or S or T or A or
       347        L or I or V or M or F or Y or W or C
W--> 349 <221> VARIANT
       350 <222> LOCATION: (2)...(2)
       351 <223> OTHER INFORMATION: Xaa at position 2 can be G or S or T or A or
       352        N or P or D or E
W--> 354 <221> VARIANT
       355 <222> LOCATION: (3)...(3)
       356 <223> OTHER INFORMATION: Xaa at position 3 can not be E or D or
       357        P or K or R or H
W--> 359 <221> VARIANT
       360 <222> LOCATION: (4)...(4)
       361 <223> OTHER INFORMATION: Xaa at position 4 can
       362        be any amino acid
W--> 364 <221> VARIANT
       365 <222> LOCATION: (5)...(5)
       366 <223> OTHER INFORMATION: Xaa at position 5 can
       367        be any amino acid
W--> 369 <221> VARIANT
       370 <222> LOCATION: (6)...(6)
       371 <223> OTHER INFORMATION: Xaa at position 6 can be L or I or V or M or
```

```
        372      N or Q or G or A
W--> 374 <221> VARIANT
        375 <222> LOCATION: (7)...(7)
        376 <223> OTHER INFORMATION: Xaa at position 7 can
        377      be any amino acid
W--> 379 <221> VARIANT
        380 <222> LOCATION: (8)...(8)
        381 <223> OTHER INFORMATION: Xaa at position 8 can
        382      be any amino acid
W--> 385 <221> VARIANT
        386 <222> LOCATION: (9)...(9)
        387 <223> OTHER INFORMATION: Xaa at position 9 can be L or I or V or M or
        388      F or T
W--> 390 <221> VARIANT
        391 <222> LOCATION: (10)...(10)
        392 <223> OTHER INFORMATION: Xaa at position 10 can be G or S or T or A or
        393      N or C
W--> 395 <221> VARIANT
        396 <222> LOCATION: (11)...(11)
        397 <223> OTHER INFORMATION: Xaa at position 11 can be L or I or V or M
        398      or F or Y or W or S or T or A or C
W--> 400 <221> VARIANT
        401 <222> LOCATION: (12)...(12)
        402 <223> OTHER INFORMATION: Xaa at position 12 can be D or E or N or H
W--> 404 <221> VARIANT
        405 <222> LOCATION: (14)...(14)
        406 <223> OTHER INFORMATION: Xaa at position 14 can be F or Y or W or C
        407      or S or H
W--> 409 <221> VARIANT
        410 <222> LOCATION: (15)...(15)
        411 <223> OTHER INFORMATION: Xaa at position 15
        412      can be any amino acid
W--> 415 <221> VARIANT
        416 <222> LOCATION: (16)...(16)
        417 <223> OTHER INFORMATION: Xaa at position 16
        418      can be any amino acid
W--> 421 <221> VARIANT
        422 <222> LOCATION: (17)...(17)
        423 <223> OTHER INFORMATION: Xaa at position 17 can be L or I or V or M
W--> 425 <400> 6
W--> 426 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa Xaa
        427 1               5                   10                  15
W--> 428 Xaa
E--> 431 ( - 1 - ) - delete
```

VERIFICATION SUMMARY   DATE: 10/25/2002
PATENT APPLICATION: US/10/085,233B   TIME: 10:31:20

Input Set : **A:\PTO.DC.txt**
Output Set: **N:\CRF4\10252002\J085233B.raw**

L:122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1325
L:344 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:349 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:354 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:359 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:364 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:369 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:374 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:379 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:385 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:390 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:395 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:400 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:404 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:409 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:415 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:421 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:425 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:428 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:16
L:431 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6